

APPENDIX

Sequence Data

Seq ID No1: DNA sequence of Fuz1

CACCCGAGCCATATGAGATCTACNCCWGCNNGNTCHGGNGARCARAAYATGATYGGNATG
ACNCCWACNGTNATYGCNGTNCACCTACCTGGACCAGACCG

Seq ID No2: DNA sequence of Fuz2

GGCCAGCTGCTGGGTRTANCCYTTYTTRATVAGYTCVAGNGCYTCYTGRGCTTYTCRAT
NCCRAAYTTYTCCCAYTGYTCGGTCTGGTCCAGG

Seq ID No 3: DNA sequence of Fuz3

CCCAGCAGCTGGCCTTYAARCARCCWTCHTCHGCNTAYGCNGCNTTYAAYAAYCGYCCWC
CWTCHACNTGGCTBACNGCCTACGTGGTCAAGG

Seq ID No 4: DNA sequence of Fuz4

CCGGCTTCTGCTTCTCCAGRATVAGCCAYTTNACNGCNCCRCVAGNACGTGDGARTCRA
TNGCRATVAGRTTNGCNGCVAGDGARAANACCTTGACACGTAGGC

Seq ID No 5: DNA sequence of Fuz5

GGAGAAGCAGAAGCCGGAYGGNGTNTTYCARGARGAYGGNCCWGTNATYCACCARGARAT
GATYGGNGGNTTYCGNAACGCCAAGGAGGCAGATG

Seq ID No 6: DNA sequence of Fuz6

GCTCCCAGGAAGGCTRTTNACYTGNCCTCRCARATRTCRGNGCYTCYTGTVAGNGCRAT
VAGNACRAANGCNGTVAGDGANACATCTGCCTCCTTGGCG

Seq ID No 7: DNA sequence of Fuz7

GCCTTCCTGGGAGCATYAAYAARGCNGGNGARTAYATYGARGCNTCHTAYATGAAYCTBC
ARCGYCCWTAYACNGTNGCNATYGCNNGGTATGCCCTGGCC

Seq ID No 8: DNA sequence of Fuz8

CTGGTCAGGCTCCTCCCARCGRTTRCGRTCYTTNGCNGTRTTVAGRAAYTTNCCNAGRTA
WGGYTCYTCVAGYTTRTTCATVAGGGCCAGGGCATAACC

Seq ID No9: DNA sequence of Fuz9

GAGGAGCCTGACCAGCARCTBTAYAAAYGTNGARGCNACNTCHTAYGCNCTBCTBGCNCTB
CTBCTBCTBAARGAYTTYGAYTCHGTGCCCCCTGTAGTGC

Seq ID No10: DNA sequence of Fuz10

GGGCCAAGGCTTGGAANACCATRAANGTNGCYTGNGTDGANCCRTANCCNCCNCCRTART
ARCGYTGyTCRTTVAGCCANCGCACTACAGGGGGC

Seq ID No 11: DNA sequence of Fuz11

CCAAGCCTTGGCCARTAYCARACNGAYGTNCCWGAYCACAARGAYCTNAAAYATGGAYGT
NTCCTTCCACCTCCCC

Seq ID No 12: DNA sequence of Fuz12.

CCCAGAGCCGGCCGGTTATCAGGATCCDGANCCNCCNCCNCCDGANCCNCCNCCNCCDGA
NCCDGADGAGGGGAGGTGGAAGG

Seq ID No 13: DNA sequence of Fuz13

GGCTGATTCTCGAGAAGCAGAAGC

Seq ID No 14: DNA sequence of Fuz14

GCTTCTGCTTCTCGAGAATCAGCC

Seq ID No 15: DNA sequence of Fuz15

GCCTTCCCGGGAGCATCAACAAGGC

Seq ID No 16: DNA sequence of Fuz16

GCCTTGTTGATGCTCCCGGAAGGC

Seq ID No 17: DNA sequence of Fuz17

GGAGCCTGATCAGCAGCTCTACAACG

Seq ID No 18: DNA sequence of Fuz18

CGTTGTAGAGCTGCTGATCAGGCTCC

Seq ID No 19: DNA sequence of Fuz19

GGGTACACCCAGCAGCTGGCC

Seq ID No 20: DNA sequence of Fuz20
GGCCAGCTGCTGGGTGTACCC

Seq ID No 21: DNA sequence of Fuz21
GGTGTTCCAAGCTTTGGCCC

Seq ID No 22: DNA sequence of Fuz22
GGGCCAAAGCTTGGAACACC

Seq ID No 23: DNA sequence of Fuz23
CACCCGAGCCATATGAG

SEQ ID No 24: DNA sequence of Fuz24
CCCAGAGCCGGCCGGTTATCAGGATCC

SEQ ID No 25 DNA sequence of Fuz25
CCCAGAGCCGGCCGGTTAGCAGGATCC

SEQ ID No26

C3dlcys amino acid sequence expressed in *E.coli*

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | Met | Ala | Ser | Gly | Ser | Thr | Pro | Ala | Gly | Ser |
| 11 | Gly | Glu | Gln | Asn | Met | Ile | Gly | Met | Thr | Pro |
| 21 | Thr | Val | Ile | Ala | Val | His | Tyr | Leu | Asp | Gln |
| 31 | Thr | Glu | Gln | Trp | Glu | Lys | Phe | Gly | Ile | Glu |
| 41 | Lys | Arg | Gln | Glu | Ala | Leu | Glu | Leu | Ile | Lys |
| 51 | Lys | Gly | Tyr | Thr | Gln | Gln | Leu | Ala | Phe | Lys |
| 61 | Gln | Pro | Ser | Ser | Ala | Tyr | Ala | Ala | Phe | Asn |
| 71 | Asn | Arg | Pro | Pro | Ser | Thr | Trp | Leu | Thr | Ala |
| 81 | Tyr | Val | Val | Lys | Val | Phe | Ser | Leu | Ala | Ala |
| 91 | Gln | Leu | Ile | Ala | Ile | Asp | Ser | His | Val | Leu |
| 101 | Cys | Gly | Ala | Val | Lys | Trp | Leu | Ile | Leu | Glu |
| 111 | Lys | Gln | Lys | Pro | Asp | Gly | Val | Phe | Gln | Glu |
| 121 | Asp | Gly | Pro | Val | Ile | His | Gln | Glu | Met | Ile |
| 131 | Gly | Gly | Phe | Arg | Asn | Ala | Lys | Glu | Ala | Asp |
| 141 | Val | Ser | Leu | Thr | Ala | Phe | Val | Leu | Ile | Ala |

151 Leu Gln Glu Ala Arg Asp Ile Cys Glu Gly
 161 Gln Val Asn Ser Leu Pro Gly Ser Ile Asn
 171 Lys Ala Gly Glu Tyr Ile Glu Ala Ser Tyr
 181 Met Asn Leu Gln Arg Pro Tyr Thr Val Ala
 191 Ile Ala Gly Tyr Ala Leu Ala Leu Met Asn
 201 Lys Leu Glu Glu Pro Tyr Leu Gly Lys Phe
 211 Leu Asn Thr Ala Lys Asp Arg Asn Arg Trp
 221 Glu Glu Pro Asp Gln Gln Leu Tyr Asn Val
 231 Glu Ala Thr Ser Tyr Ala Leu Leu Ala Leu
 241 Leu Leu Leu Lys Asp Phe Asp Ser Val Pro
 251 Pro Val Val Arg Trp Leu Asn Glu Gln Arg
 261 Tyr Tyr Gly Gly Gly Tyr Gly Ser Thr Gln
 271 Ala Thr Phe Met Val Phe Gln Ala Leu Ala
 281 Gln Tyr Gln Thr Asp Val Pro Asp His Asp
 291 Leu Asn Met Asp Val Ser Phe His Leu Pro
 301 Ser Ser Gly Ser Glu Glu Phe Cys

SEQ ID No 27

(C3d)3 amino acid sequence expressed in *E.coli*

1 Met Ala Ser Gly Ser Thr Pro Ala Gly Ser
 11 Gly Glu Gln Asn Met Ile Gly Met Thr Pro
 21 Thr Val Ile Ala Val His Tyr Leu Asp Gln
 31 Thr Glu Gln Trp Glu Lys Phe Gly Ile Glu
 41 Lys Arg Gln Glu Ala Leu Glu Leu Ile Lys
 52 Lys Gly Tyr Thr Gln Gln Leu Ala Phe Lys
 62 Gln Pro Ser Ser Ala Tyr Ala Ala Phe Asn
 72 Asn Arg Pro Pro Ser Thr Trp Leu Thr Ala
 82 Tyr Val Val Lys Val Phe Ser Leu Ala Ala
 91 Gln Leu Ile Ala Ile Asp Ser His Val Leu
 102 Cys Gly Ala Val Lys Trp Leu Ile Leu Glu
 112 Lys Gln Lys Pro Asp Gly Val Phe Gln Glu
 122 Asp Gly Pro Val Ile His Gln Glu Met Ile
 132 Gly Gly Phe Arg Asn Ala Lys Glu Ala Asp
 141 Val Ser Leu Thr Ala Phe Val Leu Ile Ala
 152 Leu Gln Glu Ala Arg Asp Ile Cys Glu Gly

162 Gln Val Asn Ser Leu Pro Gly Ser Ile Asn
172 Lys Ala Gly Glu Tyr Ile Glu Ala Ser Tyr
182 Met Asn Leu Gln Arg Pro Tyr Thr Val Ala
191 Ile Ala Gly Tyr Ala Leu Ala Leu Met Asn
202 Lys Leu Glu Glu Pro Tyr Leu Gly Lys Phe
212 Leu Asn Thr Ala Lys Asp Arg Asn Arg Trp
222 Glu Glu Pro Asp Gln Gln Leu Tyr Asn Val
232 Glu Ala Thr Ser Tyr Ala Leu Leu Ala Leu
241 Leu Leu Leu Lys Asp Phe Asp Ser Val Pro
252 Pro Val Val Arg Trp Leu Asn Glu Gln Arg
262 Tyr Tyr Gly Gly Gly Tyr Gly Ser Thr Gln
272 Ala Thr Phe Met Val Phe Gln Ala Leu Ala
282 Gln Tyr Gln Thr Asp Val Pro Asp His Asp
292 Leu Asn Met Asp Val Ser Phe His Leu Pro
301 Ser Ser Gly Ser Gly Gly Gly Gly Ser Gly
311 Gly Gly Gly Ser Gly Ser Thr Pro Ala Gly
321 Ser Gly Glu Gln Asn Met Ile Gly Met Thr
331 Pro Thr Val Ile Ala Val His Tyr Leu Asp
341 Gln Thr Glu Gln Trp Glu Lys Phe Gly Ile
351 Glu Lys Arg Gln Glu Ala Leu Glu Leu Ile
361 Lys Lys Gly Tyr Thr Gln Gln Leu Ala Phe
371 Lys Gln Pro Ser Ser Ala Tyr Ala Ala Phe
381 Asn Asn Arg Pro Pro Ser Thr Trp Leu Thr
391 Ala Tyr Val Val Lys Val Phe Ser Leu Ala
401 Ala Gln Leu Ile Ala Ile Asp Ser His Val
411 Leu Cys Gly Ala Val Lys Trp Leu Ile Leu
421 Glu Lys Gln Lys Pro Asp Gly Val Phe Gln
431 Glu Asp Gly Pro Val Ile His Gln Glu Met
441 Ile Gly Gly Phe Arg Asn Ala Lys Glu Ala
451 Asp Val Ser Leu Thr Ala Phe Val Leu Ile
461 Ala Leu Gln Glu Ala Arg Asp Ile Cys Glu
471 Gly Gln Val Asn Ser Leu Pro Gly Ser Ile
481 Asn Lys Ala Gly Glu Tyr Ile Glu Ala Ser
491 Tyr Met Asn Leu Gln Arg Pro Tyr Thr Val
501 Ala Ile Ala Gly Tyr Ala Leu Ala Leu Met
511 Asn Lys Leu Glu Glu Pro Tyr Leu Gly Lys

521 Phe Leu Asn Thr Ala Lys Asp Arg Asn Arg
531 Trp Glu Glu Pro Asp Gln Gln Leu Tyr Asn
541 Val Glu Ala Thr Ser Tyr Ala Leu Leu Ala
551 Leu Leu Leu Leu Lys Asp Phe Asp Ser Val
561 Pro Pro Val Val Arg Trp Leu Asn Glu Gln
571 Arg Tyr Tyr Gly Gly Gly Tyr Gly Ser Thr
581 Gln Ala Thr Phe Met Val Phe Gln Ala Leu
591 Ala Gln Tyr Gln Thr Asp Val Pro Asp His
601 Asp Leu Asn Met Asp Val Ser Phe His Leu
611 Pro Ser Ser Gly Ser Gly Gly Gly Gly Ser
621 Gly Gly Gly Gly Ser Gly Ser Thr Pro Ala
631 Gly Ser Gly Glu Gln Asn Met Ile Gly Met
641 Thr Pro Thr Val Ile Ala Val His Tyr Leu
651 Asp Gln Thr Glu Gln Trp Glu Lys Phe Gly
661 Ile Glu Lys Arg Gln Glu Ala Leu Glu Leu
671 Ile Lys Lys Gly Tyr Thr Gln Gln Leu Ala
681 Phe Lys Gln Pro Ser Ser Ala Tyr Ala Ala
691 Phe Asn Asn Arg Pro Pro Ser Thr Trp Leu
701 Thr Ala Tyr Val Val Lys Val Phe Ser Leu
711 Ala Ala Gln Leu Ile Ala Ile Asp Ser His
721 Val Leu Cys Gly Ala Val Lys Trp Leu Ile
731 Leu Glu Lys Gln Lys Pro Asp Gly Val Phe
741 Gln Glu Asp Gly Pro Val Ile His Gln Glu
751 Met Ile Gly Gly Phe Arg Asn Ala Lys Glu
761 Ala Asp Val Ser Leu Thr Ala Phe Val Leu
771 Ile Ala Leu Gln Glu Ala Arg Asp Ile Cys
781 Glu Gly Gln Val Asn Ser Leu Pro Gly Ser
791 Ile Asn Lys Ala Gly Glu Tyr Ile Glu Ala
801 Ser Tyr Met Asn Leu Gln Arg Pro Tyr Thr
811 Val Ala Ile Ala Gly Tyr Ala Leu Ala Leu
821 Met Asn Lys Leu Glu Glu Pro Tyr Leu Gly
831 Lys Phe Leu Asn Thr Ala Lys Asp Arg Asn
841 Arg Trp Glu Glu Pro Asp Gln Gln Leu Tyr
851 Asn Val Glu Ala Thr Ser Tyr Ala Leu Leu
861 Ala Leu Leu Leu Leu Lys Asp Phe Asp Ser
871 Val Pro Pro Val Val Arg Trp Leu Asn Glu

881 Gln Arg Tyr Tyr Gly Gly Gly Tyr Gly Ser
891 Thr Gln Ala Thr Phe Met Val Phe Gln Ala
901 Leu Ala Gln Tyr Gln Thr Asp Val Pro Asp
911 His Asp Leu Asn Met Asp Val Ser Phe His
921 Leu Pro Ser Ser Gly Ser Glu Glu Phe

SEQ. ID No 28
TATGGCTAGCG

SEQ. ID No 29
ACCGATCGCCTAG

Seq ID No 30: DNA sequence of PCR forward primer

GAATTCCTAGCTTGCTTG

Seq ID No 31: DNA sequence of PCR reverse primer

TCTAGAGTCGACCAGAC

Seq ID No 32 DNA sequence of pBC66-01

1 AAATCAATCT AAAGTATATA TGAGTAACT TGGTCTGACA GTTACCAATG
50
51 CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT CGTTCATCCA
100
101 TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG GGAGGGCTTA
150
151 CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC
200
201 TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA
250
251 GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA TTGTTGCCGG
300

301 GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC
350
351 CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT ATGGCTTCAT
400
401 TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG
450
451 TGCAAAAAAG CGGTTAGCTC CTTGCGTCCT CCGATCGTTG TCAGAAGTAA
500
501 GTTGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC
550
551 TTA CTGTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA
600
601 ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT
GCTCTTGCCC 650
651 GGCGTCAACA CGGGATAATA CCGCGCCACA TAGCAGAACT
TTAAAAGTGC 700
652 TCATCATTGGAAAACGTTCT
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACT
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tgtgtccttccacctcccca
gcagtggatctgaagagttctgaGGATCTTATTAAAGCAGAACTTGTTTATTGCAGCTTA
TAATGGTTACAAATAAAGCA
ATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGT
CCAAACTCATCAATGTATCT
TATCATGTCTGGTCGACTCTAGAACTAGTAACGACGATCAAGTGGGCATCTGGAGCGGCC
CGGCACCGCAGTGCATCATC
CCGAACAAATAATAAAAGcttATCATCGATAAGCTGTCAAACATGAGAATT

Seq ID No 33

CCAGCAGTGGATCCTGCTAGAGTTCTGAGG

Seq ID No 34

CCTCAGAACTCTAGCAGGATCCACTGCTGG

Seq ID No 35 DNA sequence of #50391

CCAGCAGTGGCTCTTCCTGCTTCTGCAGGATC

Seq ID No 36 DNA sequence of #50392

GATCCTGCAGAAGCAGGAAGAGCCACTGCTGG

Seq. ID No37 Amino acid sequence of (C3d)3 expressed in baculovirus/Sf9

| | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | Met | Ala | Leu | Trp | Met | Arg | Leu | Leu | Pro | Leu |
| 10 | Leu | Ala | Leu | Leu | Ala | Leu | Trp | Ala | Pro | Ala |
| 21 | Pro | Thr | Arg | Ala | Gly | Ser | Arg | Ser | Thr | Pro |
| 31 | Ala | Gly | Ser | Gly | Glu | Gln | Asn | Met | Ile | Gly |
| 41 | Met | Thr | Pro | Thr | Val | Ile | Ala | Val | His | Tyr |
| 51 | Leu | Asp | Gln | Thr | Glu | Gln | Trp | Glu | Lys | Phe |
| 61 | Gly | Ile | Glu | Lys | Arg | Gln | Glu | Ala | Leu | Glu |
| 71 | Leu | Ile | Lys | Lys | Gly | Tyr | Thr | Gln | Gln | Leu |
| 81 | Ala | Phe | Lys | Gln | Pro | Ser | Ser | Ala | Tyr | Ala |

91 Ala Phe Asn Asn Arg Pro Pro Ser Thr Trp
101 Leu Thr Ala Tyr Val Val Lys Val Phe Ser
111 Leu Ala Ala Gln Leu Ile Ala Ile Asp Ser
121 His Val Leu Cys Gly Ala Val Lys Trp Leu
131 Ile Leu Glu Lys Gln Lys Pro Asp Gly Val
141 Phe Gln Glu Asp Gly Pro Val Ile His Gln
151 Glu Met Ile Gly Gly Phe Arg Asn Ala Lys
161 Glu Ala Asp Val Ser Leu Thr Ala Phe Val
171 Leu Ile Ala Leu Gln Glu Ala Arg Asp Ile
181 Cys Glu Gly Gln Val Asn Ser Leu Pro Gly
191 Ser Ile Asn Lys Ala Gly Glu Tyr Ile Glu
201 Ala Ser Tyr Met Asn Leu Gln Arg Pro Tyr
211 Thr Val Ala Ile Ala Gly Tyr Ala Leu Ala
221 Leu Met Asn Lys Leu Glu Glu Pro Tyr Leu
231 Gly Lys Phe Leu Asn Thr Ala Lys Asp Arg
241 Asn Arg Trp Glu Glu Pro Asp Gln Gln Leu
251 Tyr Asn Val Glu Ala Thr Ser Tyr Ala Leu
261 Leu Ala Leu Leu Leu Leu Lys Asp Phe Asp
271 Ser Val Pro Pro Val Val Arg Trp Leu Asn
281 Glu Gln Arg Tyr Tyr Gly Gly Gly Tyr Gly
291 Ser Thr Gln Ala Thr Phe Met Val Phe Gln
301 Ala Leu Ala Gln Tyr Gln Thr Asp Val Pro
311 Asp His Asp Leu Asn Met Asp Val Ser Phe
312 His Leu Pro Ser Ser Gly Ser Glu Glu Phe

Seq ID No 38 Oligos for modification of bacterial vector pBroc413

TAT GAG ATC TCC CGG GGG ATC CTA GCG GCC GCT GCA

Seq ID No 39 Oligos for modification of bacterial vector pBroc413

GCG GCC GCT AGG ATC CCC CGG GAG ATC TCA

Seq ID No 40 Peptide for trifunctional linker

Ala Lys Ala Lys Ala Lys

Seq ID no 41)

CCACCCGAGCCGGTACCAGATCTA

Seq ID no 42

GGTAGATCTGGTACCGGCTCGGGTGG

Seq ID No 43:

CGAGCCATATGGGTACCACCCCAGC

Seq ID No 44:)

GGTTAGCAGGTACCGGAACC (Seq ID dd)

Seq ID 45 Mutagenic oligo giving addition of C-terminal cysteine

GGATCTGAAGAGTTCTGCTGAGGATCCTATTAAAGC

Seq ID 46 Mutagenic oligo giving addition of C-terminal cysteine

GCTTTAATAGGATCCTCAGCAGAACTCTTCAGATCC